



## SEQUENCE LISTING

<110> Yanovsky, Martin F.  
Liljegren, Sarah  
The Regents of the University of California

<120> Selective Control of Lignin Biosynthesis in Transgenic  
Plants

<130> 19452A-000930US

<140> US 09/978,382

<141> 2001-10-15

<150> US 60/090,649

<151> 1998-06-25

<150> US 09/339,998

<151> 1999-06-25

<160> 25

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Arabidopsis sp.

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<221> CDS

<222> (101)..(829)

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Met Gly Arg Gly Arg  
1 5

ggt cag ctg aag agg ata gag aac aag atc aat agg caa gtt act ttc 163  
Val Gln Leu Lys Arg Ile Glu Asn Lys Ile Asn Arg Gln Val Thr Phe  
10 15 20

tca aag aga agg tct ggt ttg ctc aag aaa gct cat gag atc tct gtt 211  
Ser Lys Arg Arg Ser Gly Leu Leu Lys Lys Ala His Glu Ile Ser Val  
25 30 35

ctc tgc gat gct gag gtt gct ctc atc gtc ttc tct tcc aaa ggc aaa 259  
Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe Ser Ser Lys Gly Lys  
40 45 50

ctc ttc gaa tat tcc acc gac tct tgc atg gag agg ata ctt gaa cgc 307  
Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu Arg Ile Leu Glu Arg  
55 60 65

tat gat cgc tat tta tat tca gac aaa caa ctt gtt ggc cga gac gtt 355  
Tyr Asp Arg Tyr Leu Tyr Ser Asp Lys Gln Leu Val Gly Arg Asp Val  
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TECH CENTER 1600/2900

[illegible]

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<213> Arabidopsis sp.
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His Glu Ile Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe
      35          40          45

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Ser Ser Lys Gly Lys Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu  
 50 55 60  
 Arg Ile Leu Glu Arg Tyr Asp Arg Tyr Leu Tyr Ser Asp Lys Gln Leu  
 65 70 75 80  
 Val Gly Arg Asp Val Ser Gln Ser Glu Asn Trp Val Leu Glu His Ala  
 85 90 95  
 Lys Leu Lys Ala Arg Val Glu Val Leu Glu Lys Asn Lys Arg Asn Phe  
 100 105 110  
 Met Gly Glu Asp Leu Asp Ser Leu Ser Leu Lys Glu Leu Gln Ser Leu  
 115 120 125  
 Glu His Gln Leu Asp Ala Ala Ile Lys Ser Ile Arg Ser Arg Lys Asn  
 130 135 140  
 Gln Ala Met Phe Glu Ser Ile Ser Ala Leu Gln Lys Lys Asp Lys Ala  
 145 150 155 160  
 Leu Gln Asp His Asn Asn Ser Leu Leu Lys Lys Ile Lys Glu Arg Glu  
 165 170 175  
 Lys Lys Thr Gly Gln Gln Glu Gly Gln Leu Val Gln Cys Ser Asn Ser  
 180 185 190  
 Ser Ser Val Leu Leu Pro Gln Tyr Cys Val Thr Ser Ser Arg Asp Gly  
 195 200 205  
 Phe Val Glu Arg Val Gly Gly Glu Asn Gly Gly Ala Ser Ser Leu Thr  
 210 215 220  
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<222> (7)..(753)

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 Lys Leu Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu Asn Thr Thr  
 15 20 25 30  
  
 aat cgt caa gtt act ttc tgc aaa cga cgc aat ggt ctt ctc aag aaa 144  
 Asn Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Leu Lys Lys  
 35 40 45  
  
 gct tat gaa ctc tct gtc ttg tgt gat gcc gaa gtt gcc ctc gtc atc 192  
 Ala Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Ile  
 50 55 60  
  
 ttc tcc act cgt ggc cgt ctc tat gag tac gcc aac aac agt gtg agg 240  
 Phe Ser Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn Ser Val Arg  
 65 70 75  
  
 ggt aca att gaa agg tac aag aaa gct tgt tcc gat gcc gtc aac cct 288  
 Gly Thr Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala Val Asn Pro  
 80 85 90

cct tcc gtc acc gaa gct aat act cag tac tat cag caa gaa gcc tct 336  
 Pro Ser Val Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln Glu Ala Ser  
 95 100 105 110  
 aag ctt cgg agg cag att cga gat att cag aat tca aat agg cat att 384  
 Lys Leu Arg Arg Gln Ile Arg Asp Ile Gln Asn Ser Asn Arg His Ile  
 115 120 125  
 gtt ggg gaa tca ctt ggt tcc ttg aac ttc aag gaa ctc aaa aac cta 432  
 Val Gly Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu Lys Asn Leu  
 130 135 140  
 gaa gga cgt ctt gaa aaa gga atc agc cgt gtc cgc tcc aaa aag aat 480  
 Glu Gly Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys Asn  
 145 150 155  
 gag ctg tta gtg gca gag ata gag tat atg cag aag agg gaa atg gag 528  
 Glu Leu Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg Glu Met Glu  
 160 165 170  
 ttg caa cac aat aac atg tac ctg cga gca aag ata gcc gaa ggc gcc 576  
 Leu Gln His Asn Asn Met Tyr Leu Arg Ala Lys Ile Ala Glu Gly Ala  
 175 180 185 190  
 aga ttg aat ccg gac cag cag gaa tcg agt gtg ata caa ggg acg aca 624  
 Arg Leu Asn Pro Asp Gln Gln Glu Ser Ser Val Ile Gln Gly Thr Thr  
 195 200 205  
 gtt tac gaa tcc ggt gta tct tct cat gac cag tcg cag cat tat aat 672  
 Val Tyr Glu Ser Gly Val Ser Ser His Asp Gln Ser Gln His Tyr Asn  
 210 215 220  
 cgg aac tat att ccg gtg aac ctt ctt gaa ccg aat cag caa ttc tcc 720  
 Arg Asn Tyr Ile Pro Val Asn Leu Leu Glu Pro Asn Gln Gln Phe Ser  
 225 230 235  
 ggc caa gac caa cct cct ctt caa ctt gtg taa ctcaaaacat gataacttgt 773  
 Gly Gln Asp Gln Pro Pro Leu Gln Leu Val  
 240 245  
 ttcttccct cataacgatt aagagagaga cgagagagtt cattttatat ttataacgcg 833  
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<213> Arabidopsis sp.

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 35 40 45  
 Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Ile Phe Ser  
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Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn Ser Val Arg Gly Thr
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Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala Val Asn Pro Pro Ser
85          90          95
Val Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln Glu Ala Ser Lys Leu
100        105        110
Arg Arg Gln Ile Arg Asp Ile Gln Asn Ser Asn Arg His Ile Val Gly
115        120        125
Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu Lys Asn Leu Glu Gly
130        135        140
Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys Asn Glu Leu
145        150        155        160
Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg Glu Met Glu Leu Gln
165        170        175
His Asn Asn Met Tyr Leu Arg Ala Lys Ile Ala Glu Gly Ala Arg Leu
180        185        190
Asn Pro Asp Gln Gln Glu Ser Ser Val Ile Gln Gly Thr Thr Val Tyr
195        200        205
Glu Ser Gly Val Ser Ser His Asp Gln Ser Gln His Tyr Asn Arg Asn
210        215        220
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<210> 5  
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 <222> (78)..(818)  
 <223> AGAMOUS-LIKE 5 (AGL5)

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          1          5          10

agc agc aag aag ata ggg aga ggg aag ata gag ata aag agg ata gag      158
Ser Ser Lys Lys Ile Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu
          15          20          25

aac act acg aat cgt caa gtc act ttc tgc aaa cga cgc aat ggt tta      206
Asn Thr Thr Asn Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu
          30          35          40

ctc aag aaa gct tat gag ctc tct gtc ttg tgt gac gct gag gtt gct      254
Leu Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala
          45          50          55

ctt gtc atc ttc tcc act cga ggc cgt ctc tac gag tac gcc aac aac      302
Leu Val Ile Phe Ser Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn
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ggt aac cct ccg acc atc acc gaa gct aat act cag tac tat cag caa 398
Val Asn Pro Pro Thr Ile Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln
      95                      100                     105

gag gcg tct aaa ctc cgg aga cag att cgg gac att cag aat ttg aac 446
Glu Ala Ser Lys Leu Arg Arg Gln Ile Arg Asp Ile Gln Asn Leu Asn
      110                     115                     120

aga cac att ctt ggt gaa tct ctt ggt tcc ttg aac ttt aag gaa ctc 494
Arg His Ile Leu Gly Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu
      125                     130                     135

aag aac ctt gaa agt agg ctt gag aaa gga atc agt cgt gtc cga tcc 542
Lys Asn Leu Glu Ser Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser
      140                     145                     150                     155

aag aag cac gag atg tta gtt gca gag att gaa tac atg caa aaa agg 590
Lys Lys His Glu Met Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg
      160                     165                     170

gaa atc gag ctg caa aac gat aac atg tat ctc cgc tcc aag att 'act 638
Glu Ile Glu Leu Gln Asn Asp Asn Met Tyr Leu Arg Ser Lys Ile Thr
      175                     180                     185

gaa aga aca ggt cta cag caa caa gaa tcg agt gtg ata cat caa ggg 686
Glu Arg Thr Gly Leu Gln Gln Gln Glu Ser Ser Val Ile His Gln Gly
      190                     195                     200

aca gtt tac gag tcg ggt gtt act tct tct cac cag tcg ggg cag tat 734
Thr Val Tyr Glu Ser Gly Val Thr Ser Ser His Gln Ser Gly Gln Tyr
      205                     210                     215

aac cgg aat tat att gcg gtt aac ctt ctt gaa ccg aat cag aat tcc 782
Asn Arg Asn Tyr Ile Ala Val Asn Leu Leu Glu Pro Asn Gln Asn Ser
      220                     225                     230                     235

tcc aac caa gac caa cca cct ctg caa ctt gtt tga ttcagtctaa 828
Ser Asn Gln Asp Gln Pro Pro Leu Gln Leu Val
      240                     245

cataagcttc tttctcagc ctgagatcga tctatagtgt cacctaaatg cggccgcgtc 888

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<212> PRT

<213> Arabidopsis sp.

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      20           25           30

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Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala Tyr  
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           50                  55                  60  
 Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn Ser Val Arg Gly Thr  
           65                  70                  75                  80  
 Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala Val Asn Pro Pro Thr  
                   85                  90                  95  
 Ile Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln Glu Ala Ser Lys Leu  
           100                  105                  110  
 Arg Arg Gln Ile Arg Asp Ile Gln Asn Leu Asn Arg His Ile Leu Gly  
           115                  120                  125  
 Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu Lys Asn Leu Glu Ser  
           130                  135                  140  
 Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys His Glu Met  
           145                  150                  155                  160  
 Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg Glu Ile Glu Leu Gln  
                   165                  170                  175  
 Asn Asp Asn Met Tyr Leu Arg Ser Lys Ile Thr Glu Arg Thr Gly Leu  
                   180                  185                  190  
 Gln Gln Gln Glu Ser Ser Val Ile His Gln Gly Thr Val Tyr Glu Ser  
           195                  200                  205  
 Gly Val Thr Ser Ser His Gln Ser Gly Gln Tyr Asn Arg Asn Tyr Ile  
           210                  215                  220  
 Ala Val Asn Leu Leu Glu Pro Asn Gln Asn Ser Ser Asn Gln Asp Gln  
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 Pro Pro Leu Gln Leu Val  
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<210> 8  
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27

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<210> 11  
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<400> 11  
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<210> 12  
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<400> 13  
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<210> 16  
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<400> 16  
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<210> 17  
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<220>  
 <223> Description of Artificial Sequence:PCR  
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<210> 18  
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 amplification oligonucleotide primer

<400> 18  
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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (2758)..(3354)

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(R-like bHLH)

&lt;400&gt; 24

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gaagtaatat tgatatgtat gtaataacat atctgattgc ggtaaaaaaa aacatatctg 1620

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 Pro Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn Asp Leu  
 35 40 45  
 ctc aca caa gaa cac gca gct ttt ctc aat gat cct cac cat ctc atg 2949  
 Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His Leu Met  
 50 55 60  
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 Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu Glu  
 65 70 75 80  
 tac gat gaa gac atg gat gcg atg aag gag atg cag tac atg atc gcc 3045  
 Tyr Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met Ile Ala  
 85 90 95

gtc atg cag ccc gta gac atc gac cct gcc acg gtc cct aag ccg aac 3093  
 Val Met Gln Pro Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn  
                   100                  105                  110

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 Arg Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Thr Val Val Ala Arg  
                   115                  120                  125

cgg cgt cgg gaa agg atc agc gag aag atc cga att ctc aag agg atc 3189  
 Arg Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Ile  
                   130                  135                  140

gtg cct ggt ggt gcg aag atg gac aca gct tcc atg ctc gac gaa gcc 3237  
 Val Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala  
                   145                  150                  155                  160

ata cgt tac acc aag ttc ttg aaa cgg cag gtg agg att ctt cag cct 3285  
 Ile Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu Gln Pro  
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cac tct cag att gga gct cct atg gct aac ccc tct tac ctt tgt tat 3333  
 His Ser Gln Ile Gly Ala Pro Met Ala Asn Pro Ser Tyr Leu Cys Tyr  
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 Tyr His Asn Ser Gln Pro  
                   195

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                   20                  25                  30  
 Pro Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn Asp Leu  
                   35                  40                  45  
 Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His Leu Met  
                   50                  55                  60  
 Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu Glu  
   65                  70                  75                  80

[illegible]